

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/530,512
Source: PT
Date Processed by STIC: 11/8/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/530,512

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure** your subsequent submission is saved in **ASCII** text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 11/08/2005

PATENT APPLICATION: US/10/530,512

TIME: 12:09:53

Input Set : A:\Sequence Listing.ST25.txt

Output Set : N:\CRF4\11082005\J530512.raw

3 <110> APPLICANT: Keller, Charles
 4 Ballard, Linda
 5 Lemons, Richard
 6 Ali-Osman, Francis
 8 <120> TITLE OF INVENTION: HIGH THROUGHPUT DETECTION OF GLUTATHIONE S-TRANSFERASE
 9 POLYMORPHIC ALLELES
 11 <130> FILE REFERENCE: 1321.2.83/U-2962
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/530,512
 C--> 14 <141> CURRENT FILING DATE: 2005-04-06
 16 <150> PRIOR APPLICATION NUMBER: 60/418876
 17 <151> PRIOR FILING DATE: 2002-10-15
 19 <160> NUMBER OF SEQ ID NOS: 47
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 31
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: M1F GSTM1 Forward primer
 31 <400> SEQUENCE: 1
 32 gtttcttctg cttcacgtgt tatgaaggtt c
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 23
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: M1F GSTM1 Forward primer without non-specific sequence tail
 added
 42 to promote completion of non-templated nucleotide addition.
 44 <400> SEQUENCE: 2
 45 tgcttcacgt gttatgaagg ttc
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 20
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: M1R-A GSTM1 Reverse Primer
 56 <400> SEQUENCE: 3
 57 ttgggaaggc gtccaagcac
 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 23
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:

Does Not Comply
Corrected Diskette Needed

P3

31

23

20

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\11082005\J530512.raw

```

66 <223> OTHER INFORMATION: M1R-B GSTM1 Reverse primer.
68 <400> SEQUENCE: 4
69 tctttgggaa ggcgtccaag cag                                23
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 20
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: M1R-B GSTM1 Reverse primer without non-specific sequence tail
79     added to promote completion of non-templated nucleotide addition.
81 <400> SEQUENCE: 5
82 ttgggaaggc gtccaagcag                                20
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 19
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: ACTB-A Beta-Actin Forward primer.
93 <400> SEQUENCE: 6
94 cctccctgga gaagagtac                                19
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 26
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: ACTB-B Beta-Actin Reverse primer.
105 <400> SEQUENCE: 7
106 gtttctgtgt tggcgtacag gtcttt                                26
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 20
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: ACTB-B Beta-Actin Reverse primer without non-specific
sequence
116     tail added to promote completion of non-templated nucleotide
117     addition.
119 <400> SEQUENCE: 8
120 gtgttggcgt acaggtcttt                                20
123 <210> SEQ ID NO: 9
124 <211> LENGTH: 26
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: M3F GSTM3 Forward primer.
131 <400> SEQUENCE: 9
132 gtttctcctc agtacttgga agagct                                26
135 <210> SEQ ID NO: 10
136 <211> LENGTH: 20
137 <212> TYPE: DNA

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RAW SEQUENCE LISTING

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TIME: 12:09:53

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\11082005\J530512.raw

138 <213> ORGANISM: Artificial Sequence
 140 <220> FEATURE:
 141 <223> OTHER INFORMATION: M3F GSTM3 Forward primer without non-specific sequence tail
 added
 142 to promote completion of non-templated nucleotide addition.
 144 <400> SEQUENCE: 10
 145 cctcagtact tggaagagct 20
 148 <210> SEQ ID NO: 11
 149 <211> LENGTH: 26 *invalid <2137 response see item 10*
 150 <212> TYPE: DNA *on Error Summary sheet.*
 151 <213> ORGANISM: M3R GSTM3 Reverse primer.
 153 <400> SEQUENCE: 11
 154 gtttctcaca tgaaagcctt caggtt 26
 157 <210> SEQ ID NO: 12
 158 <211> LENGTH: 20
 159 <212> TYPE: DNA
 160 <213> ORGANISM: Artificial Sequence
 162 <220> FEATURE:
 163 <223> OTHER INFORMATION: M3R GSTM3 Reverse primer without non-specific sequence tail
 added
 164 to promote completion of non-templated nucleotide addition.
 166 <400> SEQUENCE: 12
 167 cacatgaaag ccttcaggtt 20
 170 <210> SEQ ID NO: 13 *invalid*
 171 <211> LENGTH: 25
 172 <212> TYPE: DNA
 173 <213> ORGANISM: P1-104FA GSTP1 Forward primer. *please correct similar error in subsequent sequences*
 175 <400> SEQUENCE: 13
 176 gtttctgacc tccgctgcaa ataca 25
 179 <210> SEQ ID NO: 14
 180 <211> LENGTH: 19
 181 <212> TYPE: DNA
 182 <213> ORGANISM: Artificial Sequence
 184 <220> FEATURE:
 185 <223> OTHER INFORMATION: P1-104FA GSTP1 Forward primer without non-specific sequence
 tail
 186 added to promote completion of non-templated nucleotide addition.
 188 <400> SEQUENCE: 14
 189 gacctccgct gcaaataca 19
 192 <210> SEQ ID NO: 15
 193 <211> LENGTH: 28
 194 <212> TYPE: DNA
 195 <213> ORGANISM: Artificial Sequence
 197 <220> FEATURE:
 198 <223> OTHER INFORMATION: P1-104FG GSTP1 Forward primer.
 200 <400> SEQUENCE: 15
 201 gtttctcttg acctccgctg caaatagc 28
 204 <210> SEQ ID NO: 16
 205 <211> LENGTH: 19
 206 <212> TYPE: DNA
 207 <213> ORGANISM: Artificial Sequence
 209 <220> FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing.ST25.txt

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```

210 <223> OTHER INFORMATION: P1-104FG GSTP1 Forward primer without non-specific sequence
tail
211      added to promote completion of non-templated nucleotide addition.
213 <400> SEQUENCE: 16
214 gacctccgct gcaaatacg                                     19
217 <210> SEQ ID NO: 17
218 <211> LENGTH: 23
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: P1-104R GSTP1 Reverse primer.
225 <400> SEQUENCE: 17
226 gtttctcagc ccaagccacc tga                                23
229 <210> SEQ ID NO: 18
230 <211> LENGTH: 18
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: P1-104R GSTP1 Reverse primer without non-specific sequence
tail
236      added to promote completion of non-templated nucleotide addition.
238 <400> SEQUENCE: 18
239 tcagcccaag ccacctga                                     18
242 <210> SEQ ID NO: 19
243 <211> LENGTH: 27
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: P1-113FT GSTP1 Forward primer.
250 <400> SEQUENCE: 19
251 gtttctctttt ggtgtctggc aggaggt                            27
254 <210> SEQ ID NO: 20
255 <211> LENGTH: 17
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: P1-113FT GSTP1 Forward primer without non-specific sequence
tail
261      added to promote completion of non-templated nucleotide addition.
263 <400> SEQUENCE: 20
264 ggtgtctggc aggaggt                                     17
267 <210> SEQ ID NO: 21
268 <211> LENGTH: 23
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: P1-113FC GSTP1 Forward primer.
275 <400> SEQUENCE: 21
276 gtttctgggtg tctggcagga ggc                                23
279 <210> SEQ ID NO: 22
280 <211> LENGTH: 17
281 <212> TYPE: DNA

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RAW SEQUENCE LISTING

DATE: 11/08/2005

PATENT APPLICATION: US/10/530,512

TIME: 12:09:53

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\11082005\J530512.raw

```

282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: P1-113FC GSTP1 Forward primer without non-specific sequence
tail
286         added to promote completion of non-templated nucleotide addition.
288 <400> SEQUENCE: 22
289 ggtgtctggc aggaggc                                     17
292 <210> SEQ ID NO: 23
293 <211> LENGTH: 19
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: P1-113R GSTP1 Reverse primer.
300 <400> SEQUENCE: 23
301 tggctctccca caatgaagg                                     19
304 <210> SEQ ID NO: 24
305 <211> LENGTH: 23
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: T1F GSTT1 Forward primer.
312 <400> SEQUENCE: 24
313 ttccttactg gtctcacat ctc                                     23
316 <210> SEQ ID NO: 25
317 <211> LENGTH: 27
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: T1R GSTT1 Reverse primer.
324 <400> SEQUENCE: 25
325 gtttctacag actggggatg gatggtt                             27
328 <210> SEQ ID NO: 26
329 <211> LENGTH: 22
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: T1R GSTT1 Reverse primer without non-specific sequence tail
added
335         to promote completion of non-templated nucleotide addition.
337 <400> SEQUENCE: 26
338 tacagactgg ggatggatgg tt                                     22
341 <210> SEQ ID NO: 27
342 <211> LENGTH: 26
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: M2F10 forward primer.
349 <400> SEQUENCE: 27
350 aagacagagg aagggtgcat ttgata                             26
353 <210> SEQ ID NO: 28
354 <211> LENGTH: 24

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/08/2005
PATENT APPLICATION: US/10/530,512 TIME: 12:09:54

Input Set : A:\Sequence Listing.ST25.txt
Output Set: N:\CRF4\11082005\J530512.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1

VERIFICATION SUMMARY

DATE: 11/08/2005

PATENT APPLICATION: US/10/530,512

TIME: 12:09:54

Input Set : A:\Sequence Listing.ST25.txt

Output Set: N:\CRF4\11082005\J530512.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date